

SEQUENCE LISTING

<110> Zhang, Mingjie
Sucher, Nikolaus J.

<120> DRUG SCREENING METHOD FOR THE TREATMENT
OF BRAIN DAMAGE

<130> WILKG5.001AUS

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2115

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)...(2115)

<223> PSD-95

<221> misc_feature

<222> (160)...(246)

<223> PDZ2 coding sequence

<400> 1

atg gac tgt ctc tgt ata gtg aca acc aag aaa tac cgc tac caa gat	48
Met Asp Cys Leu Cys Ile Val Thr Thr Lys Lys Tyr Arg Tyr Gln Asp	
1 5 10 15	
 gaa gac acg ccc cct ctg gaa cac agc ccg gcc cac ctc ccc aac cag	96
Glu Asp Thr Pro Pro Leu Glu His Ser Pro Ala His Leu Pro Asn Gln	
20 25 30	
 gcc aat tct ccc cct gtg att gtc aac acg gac acc cta gaa gcc cca	144
Ala Asn Ser Pro Pro Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro	
35 40 45	
 gga tat gag ttg cag gtg aat gga aca gag ggg gag atg gag tat gag	192
Gly Tyr Glu Leu Gln Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu	
50 55 60	
 gag atc aca ttg gaa agg ggt aac tca ggt ctg ggc ttc agc atc gca	240
Glu Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala	
65 70 75 80	
 ggt ggc act gac aac ccg cac atc ggt gac gac ccg tcc att ttt atc	288
Gly Gly Thr Asp Asn Pro His Ile Gly Asp Asp Pro Ser Ile Phe Ile	
85 90 95	
 acc aag atc att cct ggt ggg gct gca gcc cag gat ggc cgc ctc agg	336
Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg	
100 105 110	

gtc aat gac agc atc ctg ttt gta aat gaa gtg gat gtt cgg gag gtg	384
Val Asn Asp Ser Ile Leu Phe Val Asn Glu Val Asp Val Arg Glu Val	
115 120 125	
acc cat tca gct gcg gtg gag gcc ctc aaa gag gca ggt tcc atc gtt	432
Thr His Ser Ala Ala Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val	
130 135 140	
cgc ctc tat gtc atg cgc cgg aaa ccc cca gcc gaa aag gtc atg gag	480
Arg Leu Tyr Val Met Arg Arg Lys Pro Pro Ala Glu Lys Val Met Glu	
145 150 155 160	
atc aaa ctc atc aaa ggg cct aaa gga ctt ggc ttc agc att gcg ggg	528
Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly	
165 170 175	
ggc gtt ggg aac cag cac atc cct gga gat aac agc atc tat gta acg	576
Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr	
180 185 190	
aag atc atc gaa gga ggt gct gcc cac aag gat ggc agg ttg cag att	624
Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp Gly Arg Leu Gln Ile	
195 200 205	
gga gac aag atc ctg gcg gtc aac agt gtg ggg ctg gag gac gtc atg	672
Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly Leu Glu Asp Val Met	
210 215 220	
cac gag gat gcc gtg gca gcc ctg aag aac aca tat gac gtt gtg tac	720
His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr Tyr Asp Val Val Tyr	
225 230 235 240	
cta aag gtg gcc aag ccc agc aat gcc tac ctg agt gac agc tat gct	768
Leu Lys Val Ala Lys Pro Ser Asn Ala Tyr Leu Ser Asp Ser Tyr Ala	
245 250 255	
ccc cca gac atc aca tac ccc aca gcc atg acc ccc act tcc cct cgg	816
Pro Pro Asp Ile Thr Tyr Pro Thr Ala Met Thr Pro Thr Ser Pro Arg	
260 265 270	
cgc tac tcc cct gtg gcc aag gac ctg ctg ggg gag gaa gac att ccc	864
Arg Tyr Ser Pro Val Ala Lys Asp Leu Leu Gly Glu Glu Asp Ile Pro	
275 280 285	
cgg gaa cca agg cgg atc gtg atc cat cgg ggc tcc acc ggc ctg ggc	912
Arg Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly	
290 295 300	
ttc aac atc gtg ggc ggc gag gat ggt gaa ggc atc ttc atc tcc ttc	960
Phe Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe	
305 310 315 320	
atc ctt gct ggg ggt cca gcc gac ctc agt ggg gag cta cgg aag ggg	1008
Ile Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly	
325 330 335	

gac cag atc ctg tcg gtc aat ggt gtt gac ctc cgc aat gcc agt cac	1056
Asp Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His	
340 345 350	
gaa cag gct gcc att gcc ctg aag aat gcg ggt cag acg gtc acg atc	1104
Glu Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile	
355 360 365	
atc gct cag tat aaa cca gaa gag tat agt cga ttc gag gcc aag atc	1152
Ile Ala Gln Tyr Lys Pro Glu Glu Tyr Ser Arg Phe Glu Ala Lys Ile	
370 375 380	
cat gat ctt cgg gaa cag ctc atg aat agt agc cta ggc tca ggg act	1200
His Asp Leu Arg Glu Gln Leu Met Asn Ser Ser Leu Gly Ser Gly Thr	
385 390 395 400	
gca tcc ttg cga agc aac ccc aag agg ggc ttc tac att agg gcc ctg	1248
Ala Ser Leu Arg Ser Asn Pro Lys Arg Gly Phe Tyr Ile Arg Ala Leu	
405 410 415	
ttt gat tac gac aag acc aag gac tgc ggt ttc ttg agc cag gcc ctg	1296
Phe Asp Tyr Asp Lys Thr Lys Asp Cys Gly Phe Leu Ser Gln Ala Leu	
420 425 430	
agc ttc cgc ttc ggg gat gtg ctt cat gtc att gac gct ggt gac gaa	1344
Ser Phe Arg Phe Gly Asp Val Leu His Val Ile Asp Ala Gly Asp Glu	
435 440 445	
gag tgg tgg caa gca cgg cgg gtc cac tcc gac agt gag acc gac gac	1392
Glu Trp Trp Gln Ala Arg Arg Val His Ser Asp Ser Glu Thr Asp Asp	
450 455 460	
att ggc ttc att ccc agc aaa cgg cgg gtc gag cga cga gag tgg tca	1440
Ile Gly Phe Ile Pro Ser Lys Arg Arg Val Glu Arg Arg Glu Trp Ser	
465 470 475 480	
agg tta aag gcc aag gac tgg ggc tcc agc tct gga tca cag ggt cga	1488
Arg Leu Lys Ala Lys Asp Trp Gly Ser Ser Ser Gly Ser Gln Gly Arg	
485 490 495	
gaa gac tcg gtt ctg agc tat gag acg gtg acc cag atg gaa gtg cac	1536
Glu Asp Ser Val Leu Ser Tyr Glu Thr Val Thr Gln Met Glu Val His	
500 505 510	
tat gct cgt ccc atc atc atc ctt gga ccc acc aaa gac cgt gcc aac	1584
Tyr Ala Arg Pro Ile Ile Ile Leu Gly Pro Thr Lys Asp Arg Ala Asn	
515 520 525	
gat gat ctt ctc tcc gag ttc ccc gac aag ttt gga tcc tgt gtc cct	1632
Asp Asp Leu Leu Ser Glu Phe Pro Asp Lys Phe Gly Ser Cys Val Pro	
530 535 540	
cat acg aca cgt cct aag cgg gaa tat gag ata gac ggc cgg gat tac	1680
His Thr Thr Arg Pro Lys Arg Glu Tyr Glu Ile Asp Gly Arg Asp Tyr	
545 550 555 560	
cac ttt gtc tcc tcc cgg gag aaa atg gag aag gac atc cag gca cac	1728

His	Phe	Val	Ser	Ser	Arg	Glu	Lys	Met	Glu	Lys	Asp	Ile	Gln	Ala	His		
				565					570					575			
aag	ttc	att	gag	gct	ggc	cag	tac	aac	agc	cac	ctc	tat	ggg	acc	agc	1776	
Lys	Phe	Ile	Glu	Ala	Gly	Gln	Tyr	Asn	Ser	His	Leu	Tyr	Gly	Thr	Ser		
			580					585					590				
gtc	cag	tct	gtg	cga	gag	gta	gca	gag	cag	ggg	aag	cac	tgc	atc	ctc	1824	
Val	Gln	Ser	Val	Arg	Glu	Val	Ala	Glu	Gln	Gly	Lys	His	Cys	Ile	Leu		
		595					600					605					
gat	gtc	tcg	gcc	aat	gcc	gtg	cgg	cgg	ctg	cag	gcg	gcc	cac	ctg	cac	1872	
Asp	Val	Ser	Ala	Asn	Ala	Val	Arg	Arg	Leu	Gln	Ala	Ala	His	Leu	His		
	610					615					620						
ccc	atc	gcc	atc	ttc	atc	cgt	ccc	cgc	tcc	ctg	gag	aat	gtg	cta	gag	1920	
Pro	Ile	Ala	Ile	Phe	Ile	Arg	Pro	Arg	Ser	Leu	Glu	Asn	Val	Leu	Glu		
625					630				635					640			
atc	aat	aag	cgg	atc	aca	gag	gag	caa	gcc	cgg	aaa	gcc	ttc	gac	aga	1968	
Ile	Asn	Lys	Arg	Ile	Thr	Glu	Glu	Gln	Ala	Arg	Lys	Ala	Phe	Asp	Arg		
			645					650					655				
gcc	acg	aag	ctg	gag	cag	gag	ttc	aca	gag	tgc	ttc	tca	gcc	atc	gta	2016	
Ala	Thr	Lys	Leu	Glu	Gln	Glu	Phe	Thr	Glu	Cys	Phe	Ser	Ala	Ile	Val		
			660				665					670					
gag	ggc	gac	agc	ttt	gaa	gag	atc	tat	cac	aaa	gtg	aaa	cgt	gtc	att	2064	
Glu	Gly	Asp	Ser	Phe	Glu	Glu	Ile	Tyr	His	Lys	Val	Lys	Arg	Val	Ile		
		675					680					685					
gaa	gac	ctc	tca	ggc	ccc	tac	atc	tgg	gtc	cca	gcc	cga	gag	aga	ctc	2112	
Glu	Asp	Leu	Ser	Gly	Pro	Tyr	Ile	Trp	Val	Pro	Ala	Arg	Glu	Arg	Leu		
	690					695					700						
tga																2115	
*																	

<210> 2
 <211> 704
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> PSD-95

<400> 2
 Met Asp Cys Leu Cys Ile Val Thr Thr Lys Lys Tyr Arg Tyr Gln Asp
 1 5 10 15
 Glu Asp Thr Pro Pro Leu Glu His Ser Pro Ala His Leu Pro Asn Gln
 20 25 30
 Ala Asn Ser Pro Pro Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro
 35 40 45
 Gly Tyr Glu Leu Gln Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu
 50 55 60

Glu	Ile	Thr	Leu	Glu	Arg	Gly	Asn	Ser	Gly	Leu	Gly	Phe	Ser	Ile	Ala	65	70	75	80
Gly	Gly	Thr	Asp	Asn	Pro	His	Ile	Gly	Asp	Asp	Pro	Ser	Ile	Phe	Ile	85	90	95	
Thr	Lys	Ile	Ile	Pro	Gly	Gly	Ala	Ala	Ala	Gln	Asp	Gly	Arg	Leu	Arg	100	105	110	
Val	Asn	Asp	Ser	Ile	Leu	Phe	Val	Asn	Glu	Val	Asp	Val	Arg	Glu	Val	115	120	125	
Thr	His	Ser	Ala	Ala	Val	Glu	Ala	Leu	Lys	Glu	Ala	Gly	Ser	Ile	Val	130	135	140	
Arg	Leu	Tyr	Val	Met	Arg	Arg	Lys	Pro	Pro	Ala	Glu	Lys	Val	Met	Glu	145	150	155	160
Ile	Lys	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Ala	Gly	165	170	175	
Gly	Val	Gly	Asn	Gln	His	Ile	Pro	Gly	Asp	Asn	Ser	Ile	Tyr	Val	Thr	180	185	190	
Lys	Ile	Ile	Glu	Gly	Gly	Ala	Ala	His	Lys	Asp	Gly	Arg	Leu	Gln	Ile	195	200	205	
Gly	Asp	Lys	Ile	Leu	Ala	Val	Asn	Ser	Val	Gly	Leu	Glu	Asp	Val	Met	210	215	220	
His	Glu	Asp	Ala	Val	Ala	Ala	Leu	Lys	Asn	Thr	Tyr	Asp	Val	Val	Tyr	225	230	235	240
Leu	Lys	Val	Ala	Lys	Pro	Ser	Asn	Ala	Tyr	Leu	Ser	Asp	Ser	Tyr	Ala	245	250	255	
Pro	Pro	Asp	Ile	Thr	Tyr	Pro	Thr	Ala	Met	Thr	Pro	Thr	Ser	Pro	Arg	260	265	270	
Arg	Tyr	Ser	Pro	Val	Ala	Lys	Asp	Leu	Leu	Gly	Glu	Glu	Asp	Ile	Pro	275	280	285	
Arg	Glu	Pro	Arg	Arg	Ile	Val	Ile	His	Arg	Gly	Ser	Thr	Gly	Leu	Gly	290	295	300	
Phe	Asn	Ile	Val	Gly	Gly	Glu	Asp	Gly	Glu	Gly	Ile	Phe	Ile	Ser	Phe	305	310	315	320
Ile	Leu	Ala	Gly	Gly	Pro	Ala	Asp	Leu	Ser	Gly	Glu	Leu	Arg	Lys	Gly	325	330	335	
Asp	Gln	Ile	Leu	Ser	Val	Asn	Gly	Val	Asp	Leu	Arg	Asn	Ala	Ser	His	340	345	350	
Glu	Gln	Ala	Ala	Ile	Ala	Leu	Lys	Asn	Ala	Gly	Gln	Thr	Val	Thr	Ile	355	360	365	
Ile	Ala	Gln	Tyr	Lys	Pro	Glu	Glu	Tyr	Ser	Arg	Phe	Glu	Ala	Lys	Ile	370	375	380	
His	Asp	Leu	Arg	Glu	Gln	Leu	Met	Asn	Ser	Ser	Leu	Gly	Ser	Gly	Thr	385	390	395	400
Ala	Ser	Leu	Arg	Ser	Asn	Pro	Lys	Arg	Gly	Phe	Tyr	Ile	Arg	Ala	Leu	405	410	415	
Phe	Asp	Tyr	Asp	Lys	Thr	Lys	Asp	Cys	Gly	Phe	Leu	Ser	Gln	Ala	Leu	420	425	430	
Ser	Phe	Arg	Phe	Gly	Asp	Val	Leu	His	Val	Ile	Asp	Ala	Gly	Asp	Glu	435	440	445	
Glu	Trp	Trp	Gln	Ala	Arg	Arg	Val	His	Ser	Asp	Ser	Glu	Thr	Asp	Asp	450	455	460	
Ile	Gly	Phe	Ile	Pro	Ser	Lys	Arg	Arg	Val	Glu	Arg	Arg	Glu	Trp	Ser	465	470	475	480
Arg	Leu	Lys	Ala	Lys	Asp	Trp	Gly	Ser	Ser	Ser	Gly	Ser	Gln	Gly	Arg	485	490	495	
Glu	Asp	Ser	Val	Leu	Ser	Tyr	Glu	Thr	Val	Thr	Gln	Met	Glu	Val	His	500	505	510	
Tyr	Ala	Arg	Pro	Ile	Ile	Ile	Leu	Gly	Pro	Thr	Lys	Asp	Arg	Ala	Asn				

Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn Ala
85 90

<210> 4
<211> 94
<212> PRT
<213> Rattus norvegicus

<220>
<223> PDZ2

<400> 4
Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly
1 5 10 15
Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn
20 25 30
Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp
35 40 45
Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly
50 55 60
Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr
65 70 75 80
Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn Ala
85 90

<210> 5
<211> 2304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2304)
<223> PSD-95

<221> misc_feature
<222> (203)...(289)
<223> PDZ2 coding sequence

<400> 5
atg tcc cag aga cca aga gct ccc agg tca gcc ctc tgg ctc ctg gca 48
Met Ser Gln Arg Pro Arg Ala Pro Arg Ser Ala Leu Trp Leu Leu Ala
1 5 10 15
ccc cca ctg ctg cgg tgg gca ccc cca ctc ctc aca gtg ctg cat agc 96
Pro Pro Leu Leu Arg Trp Ala Pro Pro Leu Leu Thr Val Leu His Ser
20 25 30
gac ctc ttc cag gcc ttg ctg gac atc ctg gac tat tat gag gct tcc 144
Asp Leu Phe Gln Ala Leu Leu Asp Ile Leu Asp Tyr Tyr Glu Ala Ser
35 40 45
ctc tca gag agt cag aaa tac cgc tac caa gat gaa gac acg ccc cct 192
Leu Ser Glu Ser Gln Lys Tyr Arg Tyr Gln Asp Glu Asp Thr Pro Pro

50	55	60	
ctg gag cac agc ccg gcc cac ctc ccc aac cag gcc aat tct ccc cca			240
Leu Glu His Ser Pro Ala His Leu Pro Asn Gln Ala Asn Ser Pro Pro			
65	70	75	80
gtg att gtc aac aca gat acc cta gaa gcc cca gga tat gag ttg cag			288
Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro Gly Tyr Glu Leu Gln			
	85	90	95
gtg aac ggg acc gag ggg gag atg gaa tac gag gaa atc aca ttg gaa			336
Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu Glu Ile Thr Leu Glu			
	100	105	110
agg ggt aac tca ggt ctg ggc ttc agc atc gca ggt ggc act gac aac			384
Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn			
	115	120	125
cca cac atc ggt gac gac cca tcc att ttc atc acc aag atc att cct			432
Pro His Ile Gly Asp Asp Pro Ser Ile Phe Ile Thr Lys Ile Ile Pro			
	130	135	140
ggt ggg gct gcg gcc cag gat ggc cgc ctc agg gtc aac gac agc atc			480
Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Ser Ile			
145	150	155	160
ctg ttt gta aat gaa gtg gac gtg cgc gag gtg acc cac tca gcg gcg			528
Leu Phe Val Asn Glu Val Asp Val Arg Glu Val Thr His Ser Ala Ala			
	165	170	175
gtg gaa gcc ctc aaa gag gca ggc tcc atc gtt cgc ctc tat gtc atg			576
Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Met			
	180	185	190
cgc cgg aag ccc ccg gct gag aag gtc atg gag atc aag ctc atc aag			624
Arg Arg Lys Pro Pro Ala Glu Lys Val Met Glu Ile Lys Leu Ile Lys			
	195	200	205
ggg cct aaa ggt ctt ggc ttc agc atc gca ggg ggc gta ggg aac cag			672
Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln			
	210	215	220
cac atc cca gga gat aat agc atc tat gta aca aag atc atc gaa ggg			720
His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly			
225	230	235	240
ggt gct gcc cac aag gat ggg agg ttg cag att gga gac aag atc ctg			768
Gly Ala Ala His Lys Asp Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu			
	245	250	255
gcg gtc aac agt gtg ggg cta gag gac gtc atg cat gaa gat gct gtg			816
Ala Val Asn Ser Val Gly Leu Glu Asp Val Met His Glu Asp Ala Val			
	260	265	270
gca gcc ctg aag aac acg tat gat gtt gtc tac cta aag gtg gcc aag			864
Ala Ala Leu Lys Asn Thr Tyr Asp Val Val Tyr Leu Lys Val Ala Lys			
	275	280	285

ccc agc aat gcc tac ctg agt gac agc tat gct ccc cca gac atc aca	912
Pro Ser Asn Ala Tyr Leu Ser Asp Ser Tyr Ala Pro Pro Asp Ile Thr	
290 295 300	
acc tct tat tcc cag cac ctg gac aat gag atc agt cac agc agc tac	960
Thr Ser Tyr Ser Gln His Leu Asp Asn Glu Ile Ser His Ser Ser Tyr	
305 310 315 320	
ctg ggc acc gac tac ccc aca gcc atg acc ccc act tcc cct cgg cgc	1008
Leu Gly Thr Asp Tyr Pro Thr Ala Met Thr Pro Thr Ser Pro Arg Arg	
325 330 335	
tac tct cca gtg gcc aag gac ctg ctc ggg gag gaa gac att ccc cga	1056
Tyr Ser Pro Val Ala Lys Asp Leu Leu Gly Glu Glu Asp Ile Pro Arg	
340 345 350	
gaa ccg agg cga att gtg atc cac cgg ggc tcc acg ggc ctg ggc ttc	1104
Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly Phe	
355 360 365	
aac atc gtg ggt ggc gag gac ggt gaa ggc atc ttc atc tcc ttt atc	1152
Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile	
370 375 380	
ctg gcc ggg ggc cct gca gac ctc agt ggg gag ctg cgg aag ggg gac	1200
Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp	
385 390 395 400	
cag atc ctg tcg gtc aac ggt gtg gac ctc cga aat gcc agc cat gag	1248
Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His Glu	
405 410 415	
cag gct gcc att gcc ctg aag aat gcg ggt cag acg gtc acg atc atc	1296
Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile Ile	
420 425 430	
gct cag tat aaa cca gaa gag tac agc cga ttc gag gcc aag atc cac	1344
Ala Gln Tyr Lys Pro Glu Glu Tyr Ser Arg Phe Glu Ala Lys Ile His	
435 440 445	
gac ctt cgg gaa cag ctc atg aac agc agc ctg ggc tca ggg act gcg	1392
Asp Leu Arg Glu Gln Leu Met Asn Ser Ser Leu Gly Ser Gly Thr Ala	
450 455 460	
tcc ttg cgg agc aac ccc aaa agg ggt ttc tac atc agg gcc ctg ttt	1440
Ser Leu Arg Ser Asn Pro Lys Arg Gly Phe Tyr Ile Arg Ala Leu Phe	
465 470 475 480	
gat tac gac aag acc aag gac tgc ggc ttc ctg agc cag gcc ctg agc	1488
Asp Tyr Asp Lys Thr Lys Asp Cys Gly Phe Leu Ser Gln Ala Leu Ser	
485 490 495	
ttc cgc ttt ggg gat gtg ctg cat gtc atc gat gct agt gat gag gag	1536
Phe Arg Phe Gly Asp Val Leu His Val Ile Asp Ala Ser Asp Glu Glu	
500 505 510	

tgg tgg cag gca cgg cgg gtc cac tct gac agt gag acc gac gac att	1584
Trp Trp Gln Ala Arg Arg Val His Ser Asp Ser Glu Thr Asp Asp Ile	
515 520 525	
ggg ttc atc ccc agc aaa cgg cgg gtt gag cga cga gag tgg tca agg	1632
Gly Phe Ile Pro Ser Lys Arg Arg Val Glu Arg Arg Glu Trp Ser Arg	
530 535 540	
tta aag gcc aag gac tgg ggc tcc agc tct gga tcg cag ggt cga gaa	1680
Leu Lys Ala Lys Asp Trp Gly Ser Ser Ser Gly Ser Gln Gly Arg Glu	
545 550 555 560	
gac tcg gtt ctg agc tac gag aca gtg acg cag atg gaa gtg cac tat	1728
Asp Ser Val Leu Ser Tyr Glu Thr Val Thr Gln Met Glu Val His Tyr	
565 570 575	
gct cgc ccc atc atc atc ctt ggg ccc acc aag gac cgc gcc aac gat	1776
Ala Arg Pro Ile Ile Ile Leu Gly Pro Thr Lys Asp Arg Ala Asn Asp	
580 585 590	
gat ctt ctg tcc gag ttc ccc gac aag ttt gga tcc tgt gtt ccc cat	1824
Asp Leu Leu Ser Glu Phe Pro Asp Lys Phe Gly Ser Cys Val Pro His	
595 600 605	
acg aca cgg ccc aag cgg gag tat gag ata gat ggc cgg gat tac cac	1872
Thr Thr Arg Pro Lys Arg Glu Tyr Glu Ile Asp Gly Arg Asp Tyr His	
610 615 620	
ttt gtg tcg tcc cgg gag aaa atg gag aag gac att cag gcg cac aag	1920
Phe Val Ser Ser Arg Glu Lys Met Glu Lys Asp Ile Gln Ala His Lys	
625 630 635 640	
ttc att gag gcc ggc cag tac aac agc cac ctg tat ggg acc agc gtc	1968
Phe Ile Glu Ala Gly Gln Tyr Asn Ser His Leu Tyr Gly Thr Ser Val	
645 650 655	
cag tcc gtg cga gag gtg gca gag cag ggg aag cac tgc atc ctg gat	2016
Gln Ser Val Arg Glu Val Ala Glu Gln Gly Lys His Cys Ile Leu Asp	
660 665 670	
gtc tcg gcc aat gcc gtg cgg cgg ctg cag gcg gcc cac ctg cac ccc	2064
Val Ser Ala Asn Ala Val Arg Arg Leu Gln Ala Ala His Leu His Pro	
675 680 685	
atc gcc atc ttc atc cgc ccc cgc tcc ctg gag aat gtg cta gag att	2112
Ile Ala Ile Phe Ile Arg Pro Arg Ser Leu Glu Asn Val Leu Glu Ile	
690 695 700	
aac aag cgg atc aca gag gag caa gcc cgc aaa gcc ttc gac aga gcc	2160
Asn Lys Arg Ile Thr Glu Glu Gln Ala Arg Lys Ala Phe Asp Arg Ala	
705 710 715 720	
acc aag ctg gag cag gag ttc aca gag tgc ttc tca gcc atc gtg gag	2208
Thr Lys Leu Glu Gln Glu Phe Thr Glu Cys Phe Ser Ala Ile Val Glu	
725 730 735	
ggg gac agc ttt gag gag atc tac cac aag gtg aag cgt gtc atc gag	2256

Gly Asp Ser Phe Glu Glu Ile Tyr His Lys Val Lys Arg Val Ile Glu
740 745 750

gac ctc tca ggc ccc tac atc tgg gtt cca gcc cga gag aga ctc tga 2304
Asp Leu Ser Gly Pro Tyr Ile Trp Val Pro Ala Arg Glu Arg Leu *
755 760 765

<210> 6
<211> 767
<212> PRT
<213> Homo sapiens

<220>
<223> PSD-95

<400> 6
Met Ser Gln Arg Pro Arg Ala Pro Arg Ser Ala Leu Trp Leu Leu Ala
1 5 10 15
Pro Pro Leu Leu Arg Trp Ala Pro Pro Leu Leu Thr Val Leu His Ser
20 25 30
Asp Leu Phe Gln Ala Leu Leu Asp Ile Leu Asp Tyr Tyr Glu Ala Ser
35 40 45
Leu Ser Glu Ser Gln Lys Tyr Arg Tyr Gln Asp Glu Asp Thr Pro Pro
50 55 60
Leu Glu His Ser Pro Ala His Leu Pro Asn Gln Ala Asn Ser Pro Pro
65 70 75 80
Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro Gly Tyr Glu Leu Gln
85 90 95
Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu Glu Ile Thr Leu Glu
100 105 110
Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn
115 120 125
Pro His Ile Gly Asp Asp Pro Ser Ile Phe Ile Thr Lys Ile Ile Pro
130 135 140
Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Ser Ile
145 150 155 160
Leu Phe Val Asn Glu Val Asp Val Arg Glu Val Thr His Ser Ala Ala
165 170 175
Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Met
180 185 190
Arg Arg Lys Pro Pro Ala Glu Lys Val Met Glu Ile Lys Leu Ile Lys
195 200 205
Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln
210 215 220
His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly
225 230 235 240
Gly Ala Ala His Lys Asp Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu
245 250 255
Ala Val Asn Ser Val Gly Leu Glu Asp Val Met His Glu Asp Ala Val
260 265 270
Ala Ala Leu Lys Asn Thr Tyr Asp Val Val Tyr Leu Lys Val Ala Lys
275 280 285
Pro Ser Asn Ala Tyr Leu Ser Asp Ser Tyr Ala Pro Pro Asp Ile Thr
290 295 300
Thr Ser Tyr Ser Gln His Leu Asp Asn Glu Ile Ser His Ser Ser Tyr

305					310					315					320
Leu	Gly	Thr	Asp	Tyr	Pro	Thr	Ala	Met	Thr	Pro	Thr	Ser	Pro	Arg	Arg
				325						330				335	
Tyr	Ser	Pro	Val	Ala	Lys	Asp	Leu	Leu	Gly	Glu	Glu	Asp	Ile	Pro	Arg
			340					345					350		
Glu	Pro	Arg	Arg	Ile	Val	Ile	His	Arg	Gly	Ser	Thr	Gly	Leu	Gly	Phe
		355					360					365			
Asn	Ile	Val	Gly	Gly	Glu	Asp	Gly	Glu	Gly	Ile	Phe	Ile	Ser	Phe	Ile
	370					375					380				
Leu	Ala	Gly	Gly	Pro	Ala	Asp	Leu	Ser	Gly	Glu	Leu	Arg	Lys	Gly	Asp
385					390					395					400
Gln	Ile	Leu	Ser	Val	Asn	Gly	Val	Asp	Leu	Arg	Asn	Ala	Ser	His	Glu
				405					410					415	
Gln	Ala	Ala	Ile	Ala	Leu	Lys	Asn	Ala	Gly	Gln	Thr	Val	Thr	Ile	Ile
			420					425					430		
Ala	Gln	Tyr	Lys	Pro	Glu	Glu	Tyr	Ser	Arg	Phe	Glu	Ala	Lys	Ile	His
		435					440					445			
Asp	Leu	Arg	Glu	Gln	Leu	Met	Asn	Ser	Ser	Leu	Gly	Ser	Gly	Thr	Ala
	450					455					460				
Ser	Leu	Arg	Ser	Asn	Pro	Lys	Arg	Gly	Phe	Tyr	Ile	Arg	Ala	Leu	Phe
465					470					475					480
Asp	Tyr	Asp	Lys	Thr	Lys	Asp	Cys	Gly	Phe	Leu	Ser	Gln	Ala	Leu	Ser
				485					490					495	
Phe	Arg	Phe	Gly	Asp	Val	Leu	His	Val	Ile	Asp	Ala	Ser	Asp	Glu	Glu
			500					505					510		
Trp	Trp	Gln	Ala	Arg	Arg	Val	His	Ser	Asp	Ser	Glu	Thr	Asp	Asp	Ile
		515					520						525		
Gly	Phe	Ile	Pro	Ser	Lys	Arg	Arg	Val	Glu	Arg	Arg	Glu	Trp	Ser	Arg
	530					535					540				
Leu	Lys	Ala	Lys	Asp	Trp	Gly	Ser	Ser	Ser	Gly	Ser	Gln	Gly	Arg	Glu
545					550					555					560
Asp	Ser	Val	Leu	Ser	Tyr	Glu	Thr	Val	Thr	Gln	Met	Glu	Val	His	Tyr
				565					570					575	
Ala	Arg	Pro	Ile	Ile	Ile	Leu	Gly	Pro	Thr	Lys	Asp	Arg	Ala	Asn	Asp
			580					585					590		
Asp	Leu	Leu	Ser	Glu	Phe	Pro	Asp	Lys	Phe	Gly	Ser	Cys	Val	Pro	His
		595					600					605			
Thr	Thr	Arg	Pro	Lys	Arg	Glu	Tyr	Glu	Ile	Asp	Gly	Arg	Asp	Tyr	His
	610					615					620				
Phe	Val	Ser	Ser	Arg	Glu	Lys	Met	Glu	Lys	Asp	Ile	Gln	Ala	His	Lys
625					630					635					640
Phe	Ile	Glu	Ala	Gly	Gln	Tyr	Asn	Ser	His	Leu	Tyr	Gly	Thr	Ser	Val
				645					650					655	
Gln	Ser	Val	Arg	Glu	Val	Ala	Glu	Gln	Gly	Lys	His	Cys	Ile	Leu	Asp
			660					665					670		
Val	Ser	Ala	Asn	Ala	Val	Arg	Arg	Leu	Gln	Ala	Ala	His	Leu	His	Pro
		675					680					685			
Ile	Ala	Ile	Phe	Ile	Arg	Pro	Arg	Ser	Leu	Glu	Asn	Val	Leu	Glu	Ile
	690					695					700				
Asn	Lys	Arg	Ile	Thr	Glu	Glu	Gln	Ala	Arg	Lys	Ala	Phe	Asp	Arg	Ala
705					710					715					720
Thr	Lys	Leu	Glu	Gln	Glu	Phe	Thr	Glu	Cys	Phe	Ser	Ala	Ile	Val	Glu
				725					730					735	
Gly	Asp	Ser	Phe	Glu	Glu	Ile	Tyr	His	Lys	Val	Lys	Arg	Val	Ile	Glu
			740					745					750		
Asp	Leu	Ser	Gly	Pro	Tyr	Ile	Trp	Val	Pro	Ala	Arg	Glu	Arg	Leu	
		755					760					765			

<210> 7
 <211> 292
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(292)
 <223> PDZ2 coding sequence

<400> 7
 gag aag gtc atg gag atc aag ctc atc aag ggg cct aaa ggt ctt ggc 48
 Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly
 1 5 10 15
 ttc agc atc gca ggg ggc gta ggg aac cag cac atc cca gga gat aat 96
 Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn
 20 25 30
 agc atc tat gta aca aag atc atc gaa ggg ggt gct gcc cac aag gat 144
 Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp
 35 40 45
 ggg agg ttg cag att gga gac aag atc ctg gcg gtc aac agt gtg ggg 192
 Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly
 50 55 60
 cta gag gac gtc atg cat gaa gat gct gtg gca gcc ctg aag aac acg 240
 Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr
 65 70 75 80
 tat gat gtt gtc tac cta aag gtg gcc aag ccc agc aat gcc tac ctg 288
 Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn Ala Tyr Leu
 85 90 95
 agt g 292
 Ser

<210> 8
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PDZ2

<400> 8
 Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly
 1 5 10 15
 Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn
 20 25 30
 Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp
 35 40 45

Gly	Arg	Leu	Gln	Ile	Gly	Asp	Lys	Ile	Leu	Ala	Val	Asn	Ser	Val	Gly
50					55					60					
Leu	Glu	Asp	Val	Met	His	Glu	Asp	Ala	Val	Ala	Ala	Leu	Lys	Asn	Thr
65					70					75					80
Tyr	Asp	Val	Val	Tyr	Leu	Lys	Val	Ala	Lys	Pro	Ser	Asn	Ala	Tyr	Leu
				85					90					95	
Ser															

S:\DOCS\DOH\DOH-7890.DOC
041604